RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,639
Source: IFWO
Date Processed by STIC: 3/2/07

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 03/02/2007
PATENT APPLICATION: US/10/574,639   TIME: 12:58:04

        Input Set : **N:\efs\03_02_07\10574639_efs\seqlisting.txt**
        Output Set: **N:\CRF4\03022007\J574639.raw**

```
 3 <110> APPLICANT: Thiry, Michel
 4         Dheur, Ingrid
 6 <120> TITLE OF INVENTION: Piscirickettsia Salmonis Antigens and Use Thereof
 8 <130> FILE REFERENCE: 425.1018
10 <140> CURRENT APPLICATION NUMBER: 10/574,639
11 <141> CURRENT FILING DATE: 2006-03-31
13 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/03339
14 <151> PRIOR FILING DATE: 2004-10-01
16 <150> PRIOR APPLICATION NUMBER: 2003/0743
17 <151> PRIOR FILING DATE: 2003-10-07
19 <160> NUMBER OF SEQ ID NOS: 19
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1314
25 <212> TYPE: DNA
26 <213> ORGANISM: Piscirickettsia salmonis
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1314)
33 <400> SEQUENCE: 1
34 atg aaa gta aaa atg att gtt gca gct gta gct gtt gca ggt tta aca        48
35 Met Lys Val Lys Met Ile Val Ala Ala Val Ala Val Ala Gly Leu Thr
36 1               5                   10                  15
38 gcg act gcc gca aat gcc gct gat aat ggt aag ctt caa tta caa atc        96
39 Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
40              20                  25                  30
42 aac caa ttg aag gcg caa cac act caa ctt caa cag caa gtt gct aat       144
43 Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Gln Val Ala Asn
44          35                  40                  45
46 ctg caa ggt caa ggc caa act act ggt gcc gtt cac gtt ggc gct gtt       192
47 Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
48      50                  55                  60
50 ggt ggt gaa cta atc tct gaa aat aac tac gat ggt cgt ggc tta gat       240
51 Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
52 65                  70                  75                  80
54 ctt ctt aaa tca tta gcg aaa gca ggc agc aat gca ccg tta tta act       288
55 Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
56                  85                  90                  95
58 att ggt ggt acg tta gaa gct gat gcg caa atg aac cgt aac ggt aat       336
59 Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
60                  100                 105                 110
62 gtt gga tct ggt tct act tct ggt gac cct tct ggc ctt aac tat act       384
63 Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr
```

```
64          115                   120                   125
66 gat gga act agc agt tct gca ttc tat tta gat act gca cgt att gat      432
67 Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp
68      130                   135                   140
70 atc tta gcg cat gtg aat gac tgg gtt aac ggt gaa atc tcg tat gac      480
71 Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp
72 145                   150                   155                   160
74 tta aat ggt gat agt ggt ctt cac act ggt agc ctt tta gtg ggt aac      528
75 Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn
76                   165                   170                   175
78 ctc aat caa tta cca gtt tat ggt caa atc ggt aaa ttc tac cca gat      576
79 Leu Asn Gln Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp
80                   180                   185                   190
82 gca ggt ttg ttt gaa tta gct agt gat gat gtt tat tct tct agc tta      624
83 Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu
84          195                   200                   205
86 gtc aag cgt tat ttc cgt cca gat gcg caa aat ggt gca tct gta ggc      672
87 Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly
88      210                   215                   220
90 ttc tat aaa gca ggc tta cat act tct tta act gca ttt aaa acg tct      720
91 Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser
92 225                   230                   235                   240
94 gct cca caa gct aat gct gct aac tat aac caa gca act agt gat tgg      768
95 Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp
96                   245                   250                   255
98 tct gca caa gcg gat tac act ttt aat gca ggt caa gtc aat gcc act      816
99 Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr
100                  260                   265                   270
102 ata ggt gca ggt tac tta tct aat atg gtg aat acc aat gac agc ttc     864
103 Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe
104          275                   280                   285
106 act gca aca ggt gca gga act ggt aca caa aaa gat cgg cta ccg atg     912
107 Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met
108      290                   295                   300
110 gct aat gta agc gct aag att ggc ttt ggt cca ttt gaa gcc ctt gct     960
111 Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala
112 305                   310                   315                   320
114 act tat gct caa aca tta aaa ggt ttg gcg aat act aca ggt ggt aca     1008
115 Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr
116                  325                   330                   335
118 acg aag ttg aaa gcc ttt gat tta gaa ggt gct tac cac ttc caa gct     1056
119 Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala
120          340                   345                   350
122 gtg aag ccg atg act gtg atg tta ggt tat agc cgt aca tat ggc ttt     1104
123 Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe
124          355                   360                   365
126 gat aag gtt gga cct gtt gat cag ttt att gat ggt aat act gcg att     1152
127 Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile
128      370                   375                   380
```

```
130 act atc aat aac aaa aaa gac caa tgg tta ttg ggt gta aac tct gaa    1200
131 Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Leu Gly Val Asn Ser Glu
132 385                 390                 395                 400
134 gta ttt aag aac aca acg gtt ggt ctt gag tat gcg cgt gta ggt cag    1248
135 Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln
136                 405                 410                 415
138 ctt gat agc aca ggt act gac act aac cgc tac aac gta ttg act gcg    1296
139 Leu Asp Ser Thr Gly Thr Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala
140                 420                 425                 430
142 gat atg act gtt aag ttc                                            1314
143 Asp Met Thr Val Lys Phe
144                 435
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 438
149 <212> TYPE: PRT
150 <213> ORGANISM: Piscirickettsia salmonis
152 <400> SEQUENCE: 2
154 Met Lys Val Lys Met Ile Val Ala Ala Val Ala Val Ala Gly Leu Thr
155 1               5                   10                  15
158 Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
159             20                  25                  30
162 Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Gln Val Ala Asn
163             35                  40                  45
166 Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
167     50                  55                  60
170 Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
171 65                  70                  75                  80
174 Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
175             85                  90                  95
178 Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
179             100                 105                 110
182 Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr
183             115                 120                 125
186 Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp
187     130                 135                 140
190 Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp
191 145                 150                 155                 160
194 Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn
195             165                 170                 175
198 Leu Asn Gln Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp
199             180                 185                 190
202 Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu
203     195                 200                 205
206 Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly
207     210                 215                 220
210 Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser
211 225                 230                 235                 240
214 Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp
215             245                 250                 255
```

RAW SEQUENCE LISTING   DATE: 03/02/2007
PATENT APPLICATION: US/10/574,639   TIME: 12:58:04

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt
Output Set: N:\CRF4\03022007\J574639.raw

```
218 Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr
219             260             265             270
222 Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe
223         275             280             285
226 Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met
227     290             295             300                  .
230 Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala
231 305             310             315 ·             320
234 Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr
235             325             330             335
238 Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala
239         340             345             350
242 Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe
243         355             360             365   ·
246 Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile
247     370             375             380
250 Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Leu Gly Val Asn Ser Glu
251 385             390             395             400
254 Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln
255             405             410             415
258 Leu Asp Ser Thr Gly Thr Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala
259             420             425             430
262 Asp Met Thr Val Lys Phe
263             435
266 <210> SEQ ID NO: 3      ·
267 <211> LENGTH: 1248
268 <212> TYPE: DNA
269 <213> ORGANISM: Piscirickettsia salmonis
272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)..(1248)
276 <400> SEQUENCE: 3
277 gct gat aat ggt aag ctt caa tta caa atc aac caa ttg aag gcg caa        48
278 Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile Asn Gln Leu Lys Ala Gln
279 1           5               10              15
281 cac act caa ctt caa cag caa gtt gct aat ctg caa ggt caa ggc caa        96
282 His Thr Gln Leu Gln Gln Gln Val Ala Asn Leu Gln Gly Gln Gly Gln
283             20              25              30           ·
285 act act ggt gcc gtt cac gtt ggc gct gtt ggt ggt gaa cta atc tct       144
286 Thr Thr Gly Ala Val His Val Gly Ala Val Gly Gly Glu Leu Ile Ser
287             35              40              45
289 gaa aat aac tac gat ggt cgt ggc tta gat ctt ctt aaa tca tta gcg       192
290 Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp Leu Leu Lys Ser Leu Ala
291     50              55              60
293 aaa gca ggc agc aat gca ccg tta tta act att ggt ggt acg tta gaa       240
294 Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr Ile Gly Gly Thr Leu Glu
295 65              70              75              80
297 gct gat gcg caa atg aac cgt aac ggt aat gtt gga tct ggt tct act       288
298 Ala Asp Ala Gln Met Asn Arg Asn Gly Asn Val Gly Ser Gly Ser Thr
```

```
299                 85                  90                  95
301 tct ggt gac cct tct ggc ctt aac tat act gat gga act agc agt tct      336
302 Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr Asp Gly Thr Ser Ser Ser
303                 100                 105                 110
305 gca ttc tat tta gat act gca cgt att gat atc tta gcg cat gtg aat      384
306 Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp Ile Leu Ala His Val Asn
307             ·115                 120                 125
309 gac tgg gtt aac ggt gaa atc tcg tat gac tta aat ggt gat agt ggt      432
310 Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp Leu Asn Gly Asp Ser Gly
311         130                 135                 140
313 ctt cac act ggt agc ctt tta gtg ggt aac ctc aat caa tta cca gtt      480
314 Leu His Thr Gly Ser Leu Leu Val Gly Asn Leu Asn Gln Leu Pro Val
315 145                 150                 155                 160
317 tat ggt caa atc ggt aaa ttc tac cca gat gca ggt ttg ttt gaa tta      528
318 Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp Ala Gly Leu Phe Glu Leu
319                 165                 170                 175
321 gct agt gat gat gtt tat tct tct agc tta gtc aag cgt tat ttc cgt      576
322 Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu Val Lys Arg Tyr Phe Arg
323                 180                 185                 190
325 cca gat gcg caa aat ggt gca tct gta ggc ttc tat aaa gca ggc tta      624
326 Pro Asp Ala Gln Asn Gly Ala Ser Val Gly Phe Tyr Lys Ala Gly Leu
327             195                 200                 205
329 cat act tct tta act gca ttt aaa acg tct gct cca caa gct aat gct      672
330 His Thr Ser Leu Thr Ala Phe Lys Thr Ser Ala Pro Gln Ala Asn Ala
331         210                 215                 220
333 gct aac tat aac caa gca act agt gat tgg tct gca caa gcg gat tac      720
334 Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp Ser Ala Gln Ala Asp Tyr
335 225                 230                 235                 240
337 act ttt aat gca ggt caa gtc aat gcc act ata ggt gca ggt tac tta      768
338 Thr Phe Asn Ala Gly Gln Val Asn Ala Thr Ile Gly Ala Gly Tyr Leu
339                 245                 250                 255
341 tct aat atg gtg aat acc aat gac agc ttc act gca aca ggt gca gga      816
342 Ser Asn Met Val Asn Thr Asn Asp Ser Phe Thr Ala Thr Gly Ala Gly
343         260                 265                 270
345 act ggt aca caa aaa gat cgg cta ccg atg gct aat gta agc gct aag      864
346 Thr Gly Thr Gln Lys Asp Arg Leu Pro Met Ala Asn Val Ser Ala Lys
347         275                 280                 285
349 att ggc ttt ggt cca ttt gaa gcc ctt gct act tat gct caa aca tta      912
350 Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala Thr Tyr Ala Gln Thr Leu
351     290                 295                 300
353 aaa ggt ttg gcg aat act aca ggt ggt aca acg aag ttg aaa gcc ttt      960
354 Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr Thr Lys Leu Lys Ala Phe
355 305                 310                 315                 320
357 gat tta gaa ggt gct tac cac ttc caa gct gtg aag ccg atg act gtg     1008
358 Asp Leu Glu Gly Ala Tyr His Phe Gln Ala Val Lys Pro Met Thr Val
359                 325                 330                 335
361 atg tta ggt tat agc cgt aca tat ggc ttt gat aag gtt gga cct gtt     1056
362 Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe Asp Lys Val Gly Pro Val
363             340                 345                 350
```

VERIFICATION SUMMARY   DATE: 03/02/2007
PATENT APPLICATION: **US/10/574,639**   TIME: 12:58:05

Input Set : **N:\efs\03_02_07\10574639_efs\seqlisting.txt**
Output Set: **N:\CRF4\03022007\J574639.raw**

```
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:496 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:501 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:506 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:511 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:516 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:521 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:526 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:
L:532 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (12) SEQUENCE:
L:537 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:542 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
L:547 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:552 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:557 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:562 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
```